PATENT
Docket No. 265.00260101

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

#7/A
Plunkett
8/15/02

Applicant(s):	Watowich et al.	Group Art Unit:	1632
Serial No.:	09/981,286	Examiner:	Unknown
Confirmation No.:	4993		
Filed:	October 15, 2001		

For: DRUG DISCOVERY METHODS

**PRELIMINARY AMENDMENT,
COMMUNICATION REGARDING ENTRY OF SEQUENCE LISTING,
AND PROPOSED DRAWING CORRECTIONS**

Assistant Commissioner for Patents
ATTN: Missing Parts
Washington, D.C. 20231

Dear Sir:

Prior to taking up the above-identified application for examination, please amend the application as follows:

In the Specification

Please replace the paragraph beginning at page 20, line 20, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

A1

The tat-CCD construct was produced by PCR using CCD in the pET30 vector and the primers N-TATCCD (5'ATGTACGGTCGTAAAAAACGTCGTCAGCGTCGTCGTGTCATGAAATTGGAATCTG ACA3' SEQ ID NO:35) and CBAM-VEE (5'GAATTCGGATCCTCATTACCATTGCTCGCAGTTCTCCGGAGT3' SEQ ID NO:36). The PCR product was phenol-chloroform extracted and was ligated into the pETBLUE vector. It was then transformed into NovaBlue Singles (Novagen) and plated on LB-Bluogal-IPTG-

carbenicillin-tetracycline plates. White colonies were selected for amplification, plasmid purification, and sequencing. The tat-CCD cDNA sequence was determined and is depicted in Figure 3.

A1

Please replace the paragraph beginning at page 26, line 28, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

Additional approaches to constructing the insert containing the library are also being used. One of these approaches involves annealing a negative strand of LIB (termed LIB r/c) to LIB itself. The LIB r/c sequence was (5'TCGAGGGAACCACC(MNN)mACCACCGGAG (SEQ ID NO:25)), where M= C, A. When LIB and LIB r/c were annealed, cohesive ends for BamHI and XhoI are formed. Another approach is to use Sequenase V 2.0 (USB, Cleveland, Ohio) to synthesize the negative LIB strand. The oligos for this are LIBSEQBAM (5'GCACGGATCCTCCGGTGGT(NNK)mGGTGGTTCCCTCGAGATCG (SEQ ID NO:26)) and SEQBAM Rev (5'CGATCTCGAGGGAACCATC (SEQ ID NO:27)). This sequenase product is then digested with BamHI (Promega, Madison, WI), and XhoI for insertion into the tat-CCD:BAM expression vectors.

A2

SEQUENCE LISTING

In accordance with 37 C.F.R. §1.821 et seq., a computer readable form (CRF) and written Sequence Listing for the above-captioned application are submitted herewith. Applicants request entry of same into the specification.

In accordance with 37 C.F.R. §1.821 et seq., it is respectfully submitted that the written Sequence Listing and the Computer readable form of the Sequence Listing are identical. It is further submitted that Sequence Listing does not contain new matter.

CORRECTION OF DRAWINGS

Applicants submit herewith proposed corrected drawings to replace originally filed sheets 3 and 4, which contain Figures 2B and 2C. The proposed corrections identify the sequences contained therein with the assigned SEQ ID NO. Additionally, at the bottom of Figure 2B, on the left hand side, text has inadvertently been omitted. Support for these corrections is found in SEQ ID NOS: 31, 32 and 12 of Figures 1 and 2A as originally filed. These changes are shown in red on the proposed corrected drawings submitted herewith. Approval of the proposed corrected drawings is respectfully requested.